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**Preliminary studies on the characterization of a Sri Lankan isolate of papaya ringspot virus (PRSV) genome**

Papaya ringspot virus (PRSV) is by far the most widespread and damaging virus that infects papaya in many papaya growing countries. The infected plants show growth reduction, reduced fruit set and the fruit quality; especially the flavour is adversely affected. Pathogen derived resistance has shown promise as along term solution to control the disease. Therefore, detail understanding of the PRSV genome is essential to achieve affective control methods.

The present study is focused on characterization of an isolate of PRSV in Sri Lanka. PRSV infected papaya leaves obtained from Kalutara area were used to isolate total RNA and reverse transcriptase -polymerase chain reaction (RT-PCR) was carried out with primers designed from a completely sequenced PRSV of Hawaiian origin. Only one pair of primer (F6/R6) gave an amplification product. The fragment was cloned and sequenced completely (958 nts). The 5' region (1-129 nts) contained a part of the nuclear inclusion protein a (NIa) gene and the 3' region (130- 958), corresponded to the nuclear inclusion protein b (NIb) gene coding for putative polymerase responsible for replicating of the potyviral RNA. Sequence comparison at nucleotide and amino acid level of the clone with known PRSV genomes revealed very high sequence homology at the amino acid level indicating the conserved nature of this NIb protein. Only 53% of the NIb gene has been isolated and characterized. Based on these sequence data specific primers for the Sri Lankan PRSV strain can be designed for future work to isolate and characterized genes such as the coat protein gene that can be used to develop transgenic papaya resistance to PRSV in Sri Lanka.